



Fig. 1. Models of the five fragments of HSA deduced from the albumin structure. Fragment constructs are shown as ribbons, surrounding amino acids within 5.5 Å are displayed as wireframe. Color code: subdomain IA, orange; IB, red; IIA, light magenta; IIB, magenta; IIIA, light blue; IIIB, blue. Disulfide bridges are colored yellow, and the lone Trp is shown. Drug binding site I is indicated, as proposed by Carter and Ho (1994) by a Connolly (1983) surface using a color scale from red for nonpolar amino acid residues to blue for polar ones. InsightII/Discover (Biosym) was used as molecular modeling software.

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